

FIGURE 1

REF ID: A697680

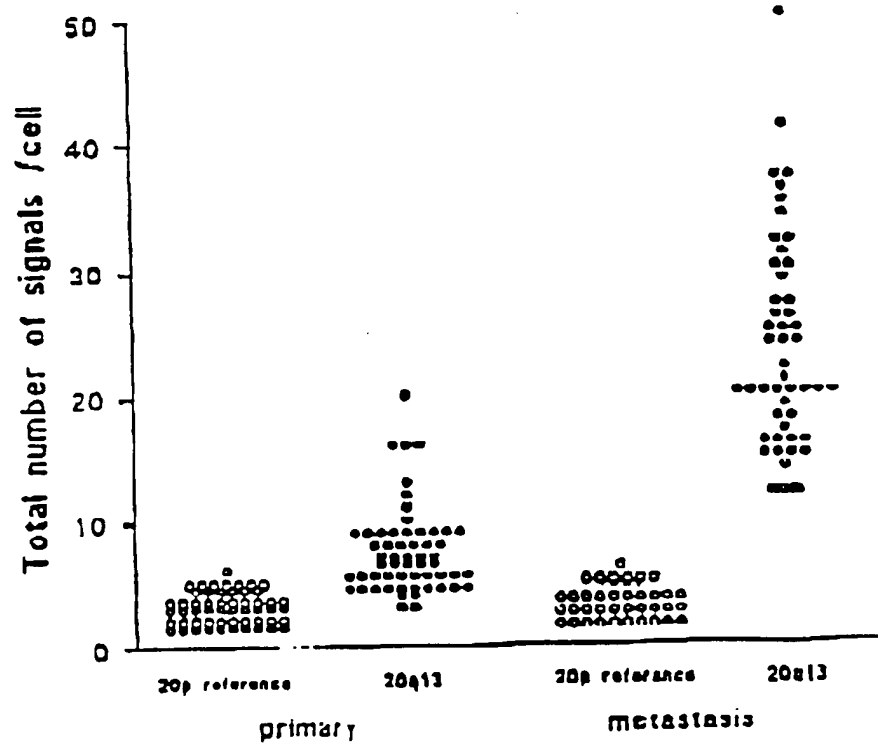


FIGURE 2

cDNAs

Even Trapped

C protein associated
 proachykinin
 Mer 137
 unique (2 ESTs)
 vitellogenin (3 ESTs)
 unique
 Alu J
 RT
 T-antigen
 unique
 retinoblastoma
 PRC protein II

Sequenced Exons

unique

unique

L1 Repeat

84513

84797

82015

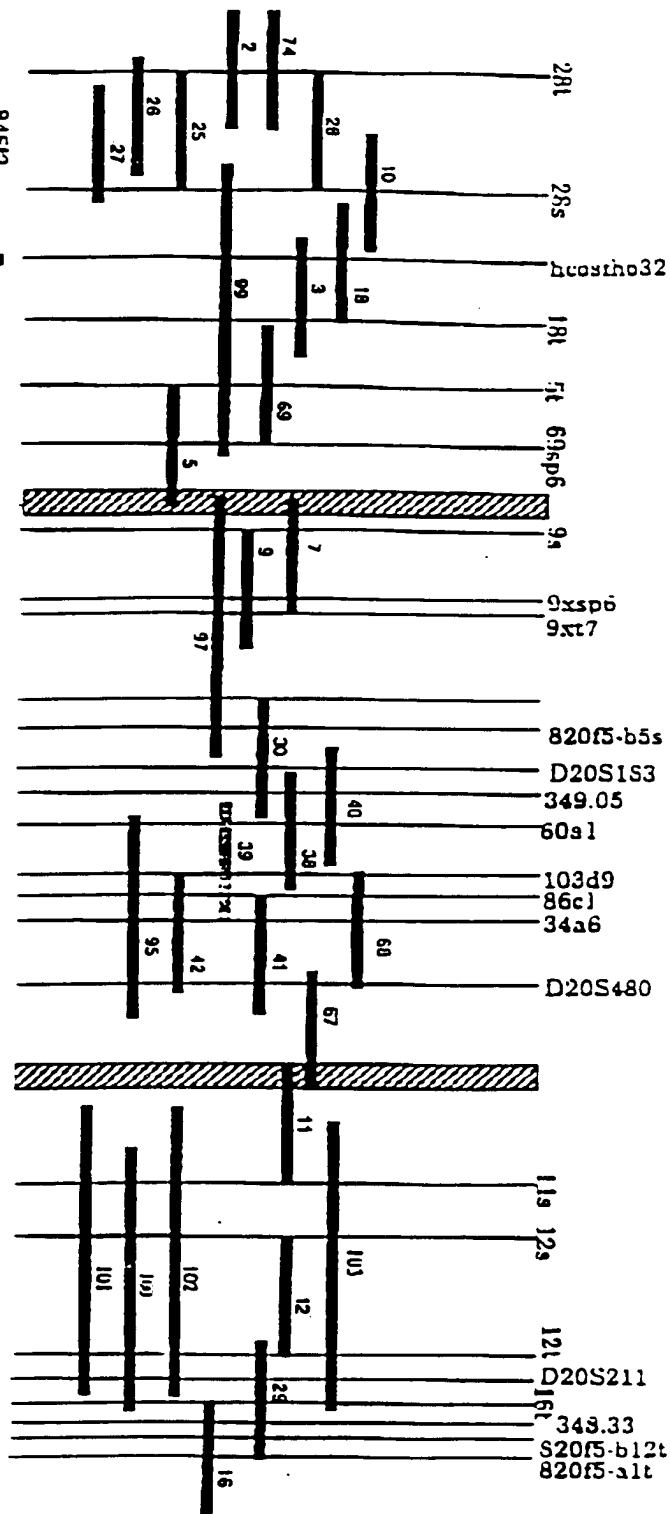


FIGURE 3

08042695.071597

08092605, 074547

1.5 Mb

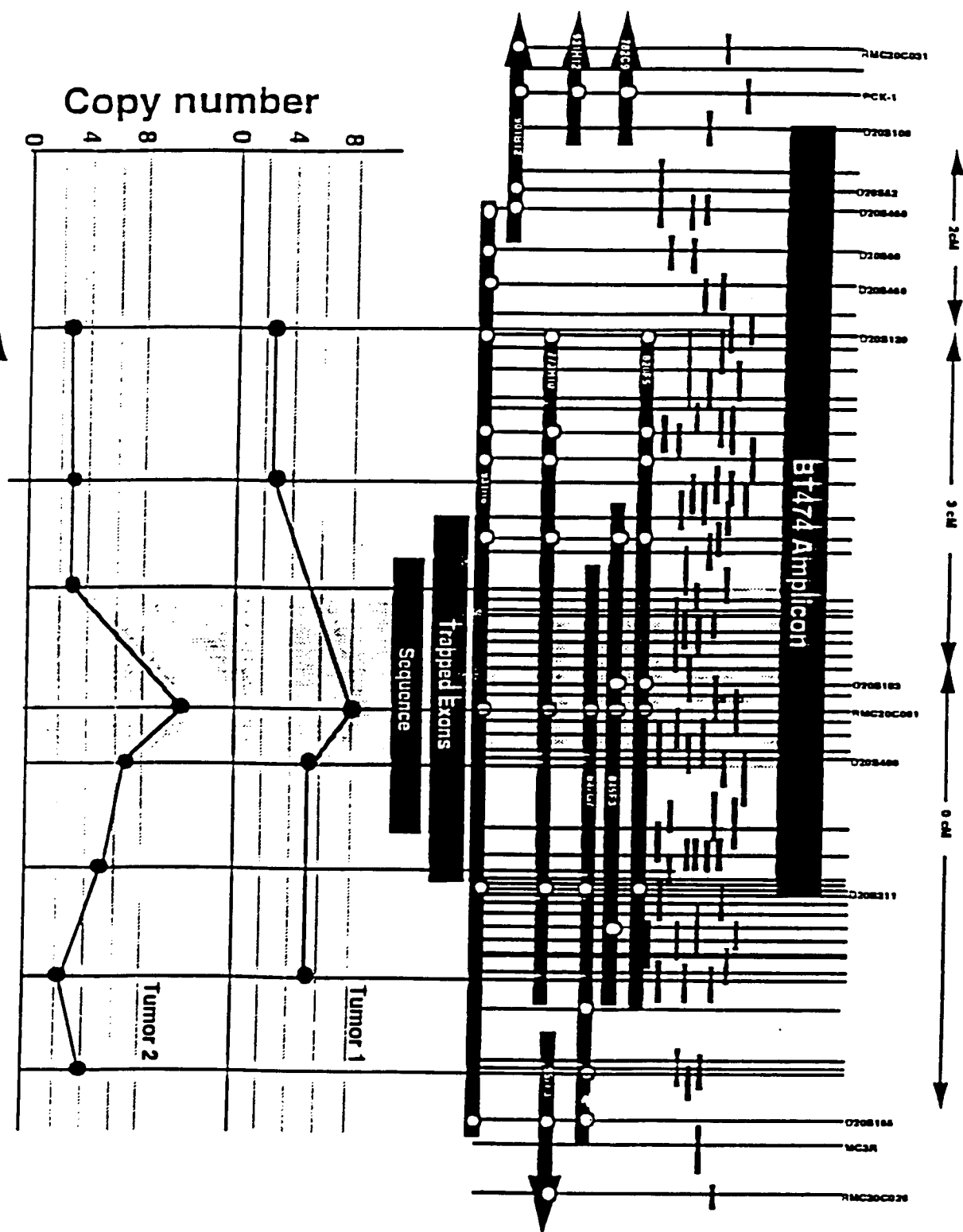


FIGURE 4

Physical map of 20913.2

RMC20C001

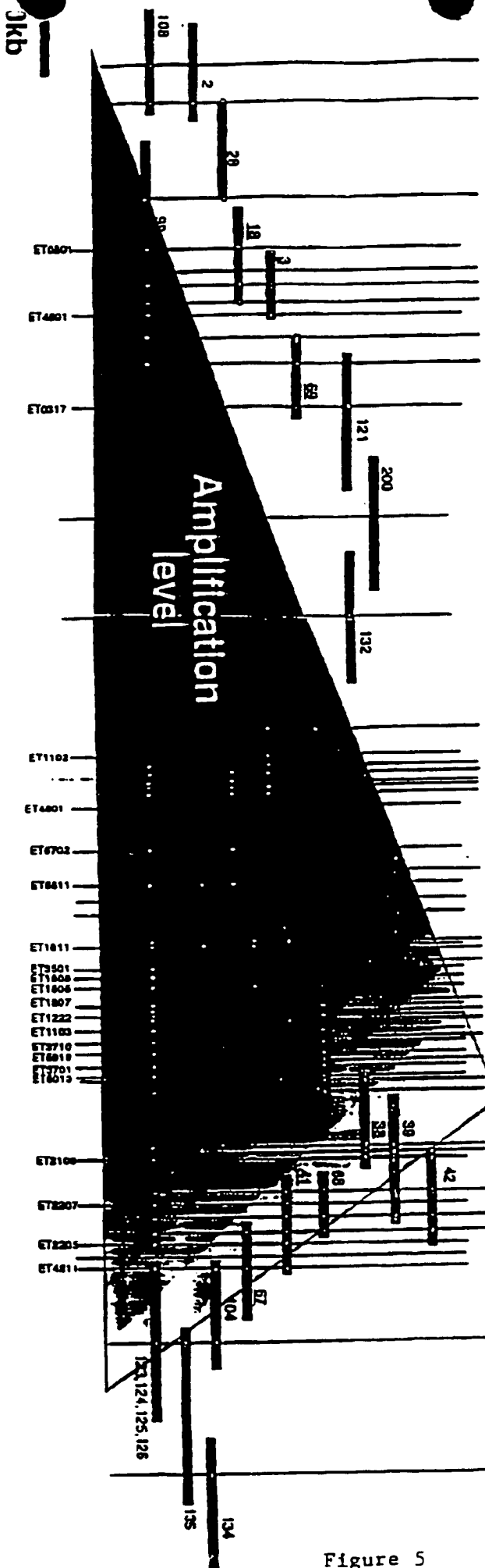


Figure 5

ene ID → 1, 2 3 4, 5 6, 7, 8, 9, 10, 11 12, 13, 14, 15

1-80X

08802695.071597

[illegible]

gb|M19533|RATCYCA Rat cyclophilin mRNA, complete cds.
Length = 743

Minus Strand HSPs:

Score = 418 (115.5 bits), Expect = 1.5e-58, Sum P(5) = 1.5e-58
Identities = 96/112 (85%), Positives = 96/112 (85%), Strand = Minus /
Plus

Query: 372 TNCAATATCACCGCAGATGGCGAGCCTTTAGGCCATGTCTCCTTCGAGCTATTTGCAGAC
313

3113
Sbjct: 64 TTCGACATCACGGCTGATGGCGAGCCCTTGGGTCGCGTCTGCTTCGAGCTGTTTGCAGAC
123

```
Query:      312 AAAGTTCCAAAGACATCAGAAACTTTCATGGTCTGAGCACTGGAGAGAAAG 261
            ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:     124 AAAGTTCCAAAGACAGCAGAAACTTTCGTGCTCTGAGCACTGGGGAGAAAG 175
```

Score = 236 (65.2 bits), Expect = 1.5e-58, Sum P(5) = 1.5e-58
Identities = 52/58 (89%), Positives = 52/58 (89%), Strand = Minus / Plus

```

Query:      117 TGCTGGACTCAACACAAATGGTTCCCAGTTTTCATCTGCACTGCCAAATCGAGTGG 60
            |||||
Subject:    348 TGCTGGACCAACACAAATGGTTCCCAGTTTTCATCTGCACTGCCAAGACTGAGTGG
            |||||
            405

```

Score = 177 (48.9 bits), Expect = 1.5e-58, Sum P(5) = 1.5e-58
Identities = 41/48 (85%), Positives = 41/48 (85%), Strand = Minus / Plus

```

Query:      60  GACTGGATGGCAAGCGTGTGATGTTTGGCAAGGTGCAAGAGGGGCATGA 13
             | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     404  GGCTGGATGGCAAGCATGTGGTCTTTGGGAAGCTCAAAGAAGGCCATGA 451

```

Score = 154 (42.6 bits), Expect = 1.5e-52, Sum P(S) = 1.5e-52
Identities = 34/38 (89%), Positives = 34/38 (89%), Strand = Minus / Plus

```

Query:      153 AGAACTTCGTTCTGAAACATGCAGGTCCTGGCATCTTG 116
              |||||
Sbjct:      299 AGAACTTCATCCTGAAGCATAACAGGTCCTGGCATCTTG 336

```

Score = 86 (23.2 bits), Expect = 1.5e-58, Sum P(5) = 1.5e-58
Identities = 22/28 (78%), Positives = 22/28 (78%), Strand = Minus / Plus

```

Query:      256 TCCTGCCTTTGCAGAATTATCCATTAT 229
             |||||
Sbjct:     193 TCCTCCTTTTCACAGAATTATCCAGGAT 220

```

Figure 6

Physical Map of 20q13.2 Breast Cancer Amplicon

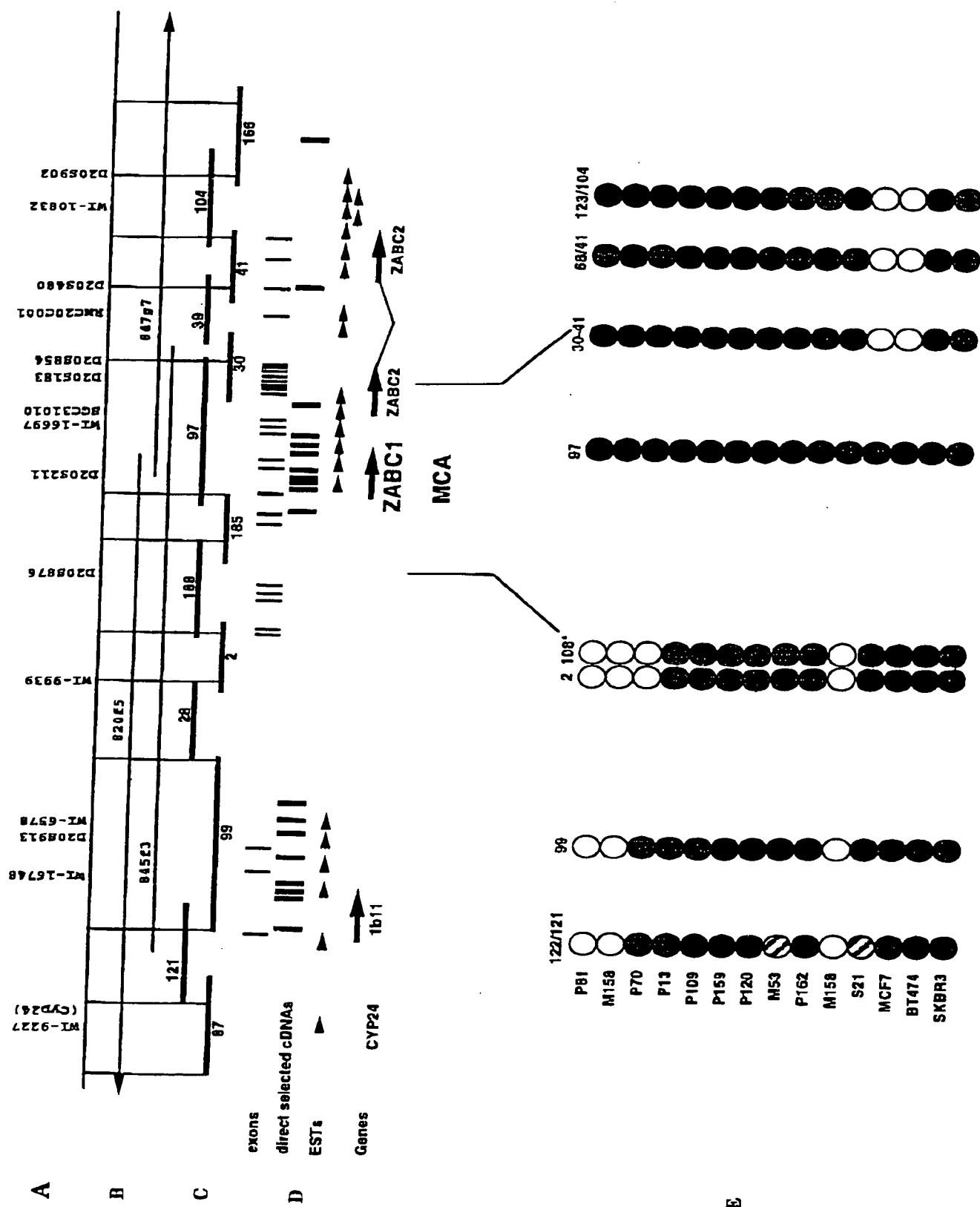


Figure 7